

Db 1 MYSLLSACTCICLHLLCFQVQMFVAEENDVDFRIVENQTRARDVSRKQRQLYOLYSR 60
 Qy 61 TSGKHLQVLGRITSARGEDGDIYQAQIIVETDFFGSQVRIGKGETEFYLICMNRKGLVGKP 120
 Db 61 TSGKHLQVLGRISAKGEDGDKYAQLIVETDFFGSQVRIGKGETEFYLICMNRKGLVGKP 120
 Qy 121 DGTSCKEVIEKVLENNYTAAMSAYSGWYVGFCKGRPRGPKTRENQQVHEMKRYPK 180
 Db 121 DGTSCKEVIEKVLENNYTAAMSAYSGWYVGFCKGRPRGPKTRENQQVHEMKRYPK 180
 Qy 181 GQPELQKPFKVTIVTAKRSRRPRTPA 207
 Db 181 GQPELQKPFKVTIVTAKRSRRPRTPA 207

RESULT 2
 057341
 ID 057341 PRELIMINARY; PRT; 210 AA.
 AC 057341;
 DT 01-JUN-1998 (TREMBLrel. 06, Created)
 DT 01-JUN-1998 (TREMBLrel. 06, Last sequence update)
 DE fibroblast growth factor 8.
 GN FGf8 OR Fgf-8 OR FGFB.
 OS Brachydanio rerio (Zebrafish) (zebra danio).
 OC Brachydanio: Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
 OC Cyprinidae; Danio.
 RN [1] SEQUENCE FROM N.A.
 RP MEDLINE#98043861; Pubmed=9334274;
 RX Fuerthauer M., Thisse C., Thisse B.;
 RT "A role for Fgf-8 in the dorsoventral patterning of the zebrafish
 gastrula.";
 RL Development; 124:4253-4264(1997).
 RN [2] SEQUENCE FROM N.A.
 RP MEDLINE#98074197; Pubmed=9609821;
 RA Reifers F., Boehni H., Walsh E.C., Crossley P.H., Stanier D.Y.R.,
 RA Brand M.;
 RT "Fgf8 is mutated in zebrafish acerebellar (ace) mutants and is
 required for maintenance of midbrain-hindbrain boundary development
 and somitogenesis.";
 RT Development 125:2381-2395(1998).
 RL EMBL; AF034264; AAC60303; 1; -.
 DR EMBL; AF034265; AAC41302; 1; -.
 HSSP; PS1371; Ig82.
 DR ZFIN; ZDB-GENE-990415-72; fgf8.
 DR InterPro; IPR002209; HB/F-growthfact.
 DR Pfam; PF00167; FGF; 1.
 DR PRODom; PD000831; HB/F-growthfact; 1.
 DR SMART; SM00442; FGF; 1.
 DR PROSITE; PS00247; HGF_FGF; UNKNOWN_1.
 SQ SEQUENCE 210 AA; 24697 MW; 9D9C3B8E18A435A CRC64;

Query Match 53.1%; Score 583; DB 13; Length 210;
 Best Local Similarity 55.9%; Pred. No. 1.7e-45;
 Matches 113; Conservative 33; Mismatches 48; Indels 8; Gaps 4;

Qy 5 PSACTCICLHLLCFQVQVLVAEENDVDFRIVENQTRARDVSRKQRQLYOLYSRTSG 64
 Db 5 PSACTCICLHLLCFQVQVLVAEENDVDFRIVENQTRARDVSRKQRQLYOLYSRTSG 64
 Qy 65 HIQVIL-GRTTSARGEDGDKYAQLLVETDFFGSQVRIGKGETEFYLICMNRKGLVGKPDGT 123
 Db 65 HIQVIL-GRTTSARGEDGDKYAQLLVETDFFGSQVRIGKGETEFYLICMNRKGLVGKPDGT 123
 Qy 64 HVQVLANKKINMAEDGVHVKLIVETDFFGSQVRIGKGETEFYLICMNRKGLVGKNGL 123
 Db 64 HVQVLANKKINMAEDGVHVKLIVETDFFGSQVRIGKGETEFYLICMNRKGLVGKNGL 123
 Qy 124 SKCYVPIEKYLENNYTAAMSAYSGWYVGFCKGRPRGPKTRENQQVHEMKRYPK 182
 Db 124 GKDCLFTEVILENNYTAAMSAYSGWYVGFCKGRPRGPKTRENQQVHEMKRYPK 183
 Qy 183 PELOPKFKTV---TKRSR 199

Db 184 IAEHRPPDFINYPFNRRKTR 205
 RESULT 3
 Q9QXQ4 PRELIMINARY; PRT; 208 AA.
 ID Q9QXQ4; PRELIMINARY;
 AC Q9QXQ4;
 DT 01-DEC-2001 (TREMBLrel. 19, Created)
 DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)
 DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)
 DE Fibroblast growth factor 8 (Fragment).
 OS Ambystoma mexicanum (Axolotl).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Amphibia; Batrachia; Caudata; Salamandroidea; Ambystomatidae;
 OC Ambystoma.
 RN [1] NCBI_TaxID=8296;
 RP SEQUENCE FROM N.A.
 RX MEDLINE#21439472; PubMed=11555861;
 RA Christensen R.N., Weinstein M., Tassava R.A.;
 RT "Fibroblast growth factors in regenerating limbs of Ambystoma: Cloning
 and semi-quantitative RT-PCR expression studies.";
 RL J. Exp. Zool. 250:525-540(2001).
 DR EMBL; AF360985; AAU16958; 1; -.
 DR InterPro; IPR002209; HB/F-growthfact.
 DR Pfam; PF00167; FGF; 1.
 DR PRODom; PD000831; HB/F-growthfact; 1.
 DR PROSITE; PS00247; HBGF_FGF; UNKNOWN_1.
 FT NON_TER 1
 FT NON_TER 208 208 MW; 9D32A77442AB70E CRC64;
 SQ SEQUENCE 208 AA; 23977 MW; 9D32A77442AB70E CRC64;

Query Match 52.7%; Score 578; DB 13; Length 208;
 Best Local Similarity 55.4%; Pred. No. 4.9e-45;
 Matches 112; Conservative 34; Mismatches 50; Indels 6; Gaps 3;

Qy 4 APSACTCLHLLCFQVQVLVAEENDVDFRIVENQTRARDVSRKQRQLYOLYSRTSG 63
 Db 7 ASSVGYLLHLFLVLCMQAVTV-OSPPNFTQHVBQSOVSYLDQSLRRLLRHYOLYSRPSG 65
 Qy 64 KHIQVIG-RRSARGEDGDKYAQLLVETDFFGSQVRIGKGETEFYLICMNRKGLVGKPDGT 122
 Db 66 KHVQVLGNKINAMADGDSHAKLIVETDFFGSQVRIGKGETEFYLICMNRKGLVGKNSG 125
 Qy 123 TSKECVIEKVLENNYTAAMSAYSGWYVGFCKGRPRGPKTRENQQVHEMKRYPK 181
 Db 126 RGKDCVFSEVLENNYTAQNLAKYEGWIAFRKGPRGSKTRHOREVHEMKRLPKGH 185
 Qy 182 --QPELQKPFKVTIVTAKRSR 200
 Db 186 QTTEPHRFEEFVNYPENRCSR 207

RESULT 4
 Q9DE51
 ID Q9DE51 PRELIMINARY; PRT; 212 AA.
 AC Q9DE51;
 DT 01-MAR-2001 (TREMBLrel. 16, Created)
 DT 01-MAR-2001 (TREMBLrel. 16, Last sequence update)
 DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)
 DE fibroblast growth factor 8.
 FGF-8
 OS Ambystoma mexicanum (Axolotl).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Amphibia; Batrachia; Caudata; Salamandroidea; Ambystomatidae;
 OC Ambystoma.
 RN NCBI_TaxID=8296;
 [1]
 RP SEQUENCE FROM N.A.
 RA Han M.J., Chung H.M., Nham S.U., Kim W.S.;
 RT "Partial cloning of FGF-8 cDNA in Mexican axolotl, Ambystoma
 mexicanum.";

DR HSSP; P31371; 1682.
 AC PRELIMINARY; PRT; 200 AA.
 DT P79925; 1997 (TREMBrel. 03, Created)
 DT 01-MAY-1997 (TREMBrel. 03, last sequence update)
 DT 01-JUN-2002 (TREMBrel. 21, last annotation update)
 DE Fibroblast growth factor 8 (fragment).
 GN FGF-8.
 OS Xenopus laevis (African clawed frog).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
 OC Xenopodinae; Xenopus.
 OX NCBI_TAXID=8355;
 RN [1]
 SEQUENCE FROM N.A.
 RX MEDLINE:98104348; PubMed-9441681;
 RA Christen B.; Slack J.M.W.;
 RT "FGF-8 Is Associated with Anteroposterior Patterning and Limb
 Regeneration in Xenopus"; Dev. Biol. 192:455-466(1997).
 RL EMBL: Y10312; CAA13651; -.
 DR HSSP; P31371; 1682.
 DR InterPro; IPR002209; HB/F-growthfact.
 DR InterPro; IPR002348; HB/F-growthfact.
 DR Pfam; PF00167; FGF; 1.
 DR PRINTS; PR00526; ILLHBGF.
 DR PRODOM; PD00831; HB/F-growthfact; 1.
 DR SMART; SM0442; FGF; 1.
 DR PROSITE; PS00247; HBGF_FGF; UNKNOWN_1.
 FT NON_TER 182 AA; 20702 MW; 1EF82473824A8D0C CRC64;
 SQ SEQUENCE 200 AA; 23453 MW; AB3C6B51C5ED5C7A CRC64;

Query Match 50.7%; Score 556.5; DB 13; Length 200;
 Best Local Similarity 53.8%; Pred. No. 4.3e-43; Indels 1; Gaps 1;
 Matches 106; Conservative 34; Mismatches 40; Gaps 4;

QY 11 LCLWFLFLCFOVOLVAVENNDVFRHVNQTYRDRDVSRKQLYQYSRTSGKHQWL- 69
 Db 11 LILHFVLCIQAQ-----HVREQLSYMDHQSLRRILRYQLYSRTSGKHQWL 58
 QY 70 GRRISAREDGGIVAQQLVETDFTGSQVRIGKETEFLCMNKKGLVKVGPKPGTSKECVF 129
 Db 59 NKKINAMADEGDPHAKLIVETDFTGSVRVIRKAETGYVYICMNKKGLKGKLGKHTNGRKOCV 118
 QY 130 IEKVLENNITALMSAKVSGWVVFPTKKGRPRKGPKTRNQDVHFMKRYPKQQ-PELQK 187
 Db 119 SETVLENNITYTALQNVKGFWMAFTRQRGPRGSKTROHQREVHFMKRLPKGHHTEPHK 178
 QY 188 PEKYTT-VTKRSRRIR 202
 Db 179 RFFFINYPFNRSKRTR 195

RESULT 8

ID Q9P78 PRELIMINARY; PRM; 182 AA.
 AC Q9P78; PRELIMINARY; PRM; 182 AA.
 DT 01-MAY-2000 (TREMBrel. 13, Created)
 DT 01-MAY-2000 (TREMBrel. 13, Last sequence update)
 DT 01-JUN-2002 (TREMBrel. 21, Last annotation update)
 DE Fgf8 (fragment).
 OS Oryzias latipes (Medaka fish).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
 OC Acanthomorpha; Acanthopterigii; Percomorpha; Atherinomorpha;
 OC Beloniformes; Adrianichthyidae; Oryziinae; Oryzias.
 OX NCBI_TAXID=8090;
 RN [1]
 SEQUENCE FROM N.A.
 RA Carl M.; Wittbrodt J.;
 RT "Graded interference with FGF-signalling uncovers its dorso-ventral asymmetry at the mid-hindbrain boundary"; Submitted (JUN-1999) to the EMBL/GenBank/DDBJ databases.
 RL EMBL; A1243210; CAB63494.1; -.

RESULT 9

ID Q9P780 PRELIMINARY; PRM; 181 AA.
 AC Q9P780; PRELIMINARY; PRM; 181 AA.
 DT 01-DEC-2001 (TREMBrel. 19, Created)
 DT 01-DEC-2001 (TREMBrel. 19, Last sequence update)
 DT 01-JUN-2002 (TREMBrel. 21, Last annotation update)
 DE LJGf8 (Fragment).
 GN LjGf8.
 OS Lampetra japonica (Japanese lamprey) (*Entosphenus japonicus*).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Hyperoartia;
 OC Peiromyzontiformes; Peiromyzontidae; Deltenteron.
 OX NCBI_TAXID=94989;
 RN [1]
 SEQUENCE FROM N.A.
 RA Shigetani Y., Sugahara F., Kawakami Y., Murakami Y., Hirano S.,
 RA Kuratani S.;
 RT "Shape precesses structure: an exaptation for the vertebrate jaw evolution";
 RT Submitted (SEP-2001) to the EMBL/GenBank/DDBJ databases.
 DR EMBL; AB071692; BAB68397.1; -.
 DR InterPro; IPR002209; HB/F-growthfact.
 DR Pfam; PF00167; FGF; 1.
 DR PRODOM; PD00831; HB/F-growthfact; 1.
 DR PROSITE; PS00247; HBGF_FGF; UNKNOWN_1.
 FT NON_TER 181 AA; 20920 MW; 8FF40A6764CE663DC CRC64;

Query Match 37.0%; Score 406; DB 13; Length 181;
 Best Local Similarity 57.7%; Pred. No. 2.2e-29;
 Matches 75; Conservative 25; Mismatches 28; Indels 2; Gaps 1;

QY 74 SARGEDSDKYAQQLVETDFTGSQVRIGKETEFLCMNKKGLVKVGPKPGTSKECVFIEKV 133
 Db 1 NARADDGKNAFKLIVETDFTGSVRVIRKAEGSYVYICMNKKGLVKVGKREGKDTCVFKETIV 60
 QY 134 LENNYTALMSAKVSGWVGFKKGRKGPKTRENQDVHFMKRYPKQQBLQKF--KY 191
 Db 61 LENNYTALLESVAGWVGFTRKGRPRGSKTSQHQREVHFMKRFORTSEERERKFIQVA 120
 QY 192 TTVTKRSRRIR 201
 Db 121 TGAARRSKRM 130

DR Pfam; PRO0167; FGF; 1.
 DR PRODom; PD00831; HB/F-growthfact; 1.
 SEQ SEQUENCE 350 AA; 40065 MW; 567DF656BD45CCC CRC64;

Query Match 18.0%; Score 197.5; DB 5; Length 350;
 Best Local Similarity 37.6%; Pred. No. 5.3e-10;
 Matches 41; Conservative 21; Mismatches 38; Indels 9; Gaps 2;

QY 84 QQLVETDFFGFSQVRIGKETEFLCMNRKGKLVGKPGDTSK---ECVFIEKVLENNYTA 140
 |::: ; :|| ; ||| ||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
 Db 22 AKMAILSTSFGRIMIQGVETGRVLCMNRKGKLVGKVLRAKHDLCOFNDLMPNLFDY 81
 | :||| | :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
 QY 141 LMAKYSWYGTTKGGPRKGKTFREMQDQHFMKR----YPKGQ 183
 | :||| | :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
 Db 82 FTNVAHPKWYAFNNSHGRKKPQPTKLQVETMPLKRIETFGPSGAP 130
 | :||| | :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||

RESULT 14

Q9PVY1	PRELIMINARY;	PRT;	208 AA.	
ID	Q9PVY1	SEQUENCE FROM N.A.	[1]	
AC	Q9PVY1;	Best Local Similarity	30.9%;	
DT	01-MAY-2000 (TREMBlrel. 13, Last sequence update)	Pred. No.	1.9e-08;	
DT	01-JUN-2002 (TREMBlrel. 21, Last annotation update)	Mismatches	54;	
DE	XFGF-20.	Indels	24;	
OS	Xenopus laevis (African clawed frog).	Gaps	8;	
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;	QY 12 CLHFLLCFOVQL---VAEENVDFRTH--ENQRARDVSKRQLRQLYOLYSRTSGH 65 : : : : : : : : : : : : : : : Db 18 CFHICLVLGFTISLACNDMTPPEOMATVNVCSSPERRHTSYDYMEGGDIRVRLFCRQWY- 76 OC Xenopidae; Xenopus.	Sequence	186 AA;
OX	XCBLTAXID=8355;	QY 66 IQVLGRRIASRG-----EDGKYAQQLVETDFFGFSQVRIGKETEFLCMNRKGKLVGK 119 : : : : : : : : : : : : : : : DR XFGF-20.	Non_TER	186
RP	SEQUENCE FROM N.A.	Db 77 -----LRDKRGKVKGQEMKSYNINMEIRIVAGI-WAIKGVESVYANNKEGKLYAK 130 MEDLINE-993151; PubMed-10441498;	SEQUENCE	186 AA;
RX	Koga C., Adati N., Nakata K., Mikoshiba K., Furuhata Y., Sato S.,	QY 120 PGTSKEVIEKVLENNYTA 170 Tei H., Sakai I., Kurokawa T., Shiokawa K., Yokoyama K.K.;	Job time	: 45 secs
RA	"Characterization of a novel member of the FGF family, xFGF-20, in	Db 131 KE-CNEDONFKELILENNYNTASAKWTHSGGEMFALLNQKGPVRKTRKEQK 184 Xenopus laevis.";	Search completed:	April 27, 2003, 14:45:56
RT	Biochem. Biophys. Res. Commun. 261:756-765(1999).	QY 100 KRETEFLCMNRKGKLVGKPGDTSKRKCVFTRKLENNTYTA 153 DR InterPro; IPR002209; HB/F-growthfact.	Job time	: 45 secs
RL	InterPro; IPR002248; IIL_HBGF.	Db 108 RGDVTGLYLGMDKRGELFGSERKLS-ECIFRQEFEENWNTYSSNLKHGDSGRRYFVAL 166 Pfan; PRO0167; FGF; 1.	Search completed:	April 27, 2003, 14:45:56
DR	PRINTS; PRO0262; IIL_HBGF.	QY 154 TIKKGRPKKGPKRKENQDVHFMKR- YPKQGPLOQ 187 SMART; SM00442; FGF; 1.	Job time	: 45 secs
DR	PROSITE; PS00247; HBGF_FGF; 1.	Db 167 NRDGTPRDGTRAKRHOKEHTFLPVPVKEVLYK 202 SEQUENCE 208 AA;	Search completed:	April 27, 2003, 14:45:56
SQ	SEQUENCE 208 AA;	QY 155 AADDVSKRQ- IRLQQLXRSRFGKHQIVL-GRRISARGEDGKRYAQQLVETDFFGFSQVRI 99 DR 43 AADDVSKRQ- IRLQQLXRSRFGKHQIVL-GRRISARGEDGKRYAQQLVETDFFGFSQVRI 99 : : : : : : : : : : : : : : : DB 50 ASPLSLHQIGIIRRQIYCRT-GFHQLQILPDQCNQVGFTQRQDHISRFQFILEFISVAIG-LVSI 107 QY 100 KRETEFLCMNRKGKLVGKPGDTSKRKCVFTRKLENNTYTA 153 : : : : : : : : : : : : : : DR 108 RGDVTGLYLGMDKRGELFGSERKLS-ECIFRQEFEENWNTYSSNLKHGDSGRRYFVAL 166 QY 154 TIKKGRPKKGPKRKENQDVHFMKR- YPKQGPLOQ 187 DR 167 NRDGTPRDGTRAKRHOKEHTFLPVPVKEVLYK 202	Job time	: 45 secs

RESULT 15

Q95L47	PRELIMINARY;	PRT;	186 AA.
ID	Q95L47	Best Local Similarity	37.2%;
AC	Q95L47;	Pred. No.	9.2e-09;
DT	01-DEC-2001 (TREMBlrel. 19, Created)	Mismatches	58;
DT	01-DEC-2001 (TREMBlrel. 19, Last sequence update)	Indels	63;
Matches	14;	Gaps	8;

QY 43 AADDVSKRQ- IRLQQLXRSRFGKHQIVL-GRRISARGEDGKRYAQQLVETDFFGFSQVRI 99
 | :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
 DB 50 ASPLSLHQIGIIRRQIYCRT-GFHQLQILPDQCNQVGFTQRQDHISRFQFILEFISVAIG-LVSI 107
 QY 100 KRETEFLCMNRKGKLVGKPGDTSKRKCVFTRKLENNTYTA 153
 | :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
 DR 108 RGDVTGLYLGMDKRGELFGSERKLS-ECIFRQEFEENWNTYSSNLKHGDSGRRYFVAL 166
 QY 154 TIKKGRPKKGPKRKENQDVHFMKR- YPKQGPLOQ 187
 DR 167 NRDGTPRDGTRAKRHOKEHTFLPVPVKEVLYK 202